Amino Acid Sequence of EGIII

MKFLQVLPALIPAALAQTSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGAHADW
QWSGGQNNVKSYQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVT
YSGDYELMIWLGKYGDIGPIGSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDV
KNFFNYLRDNKGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASIN

FIGURE 1

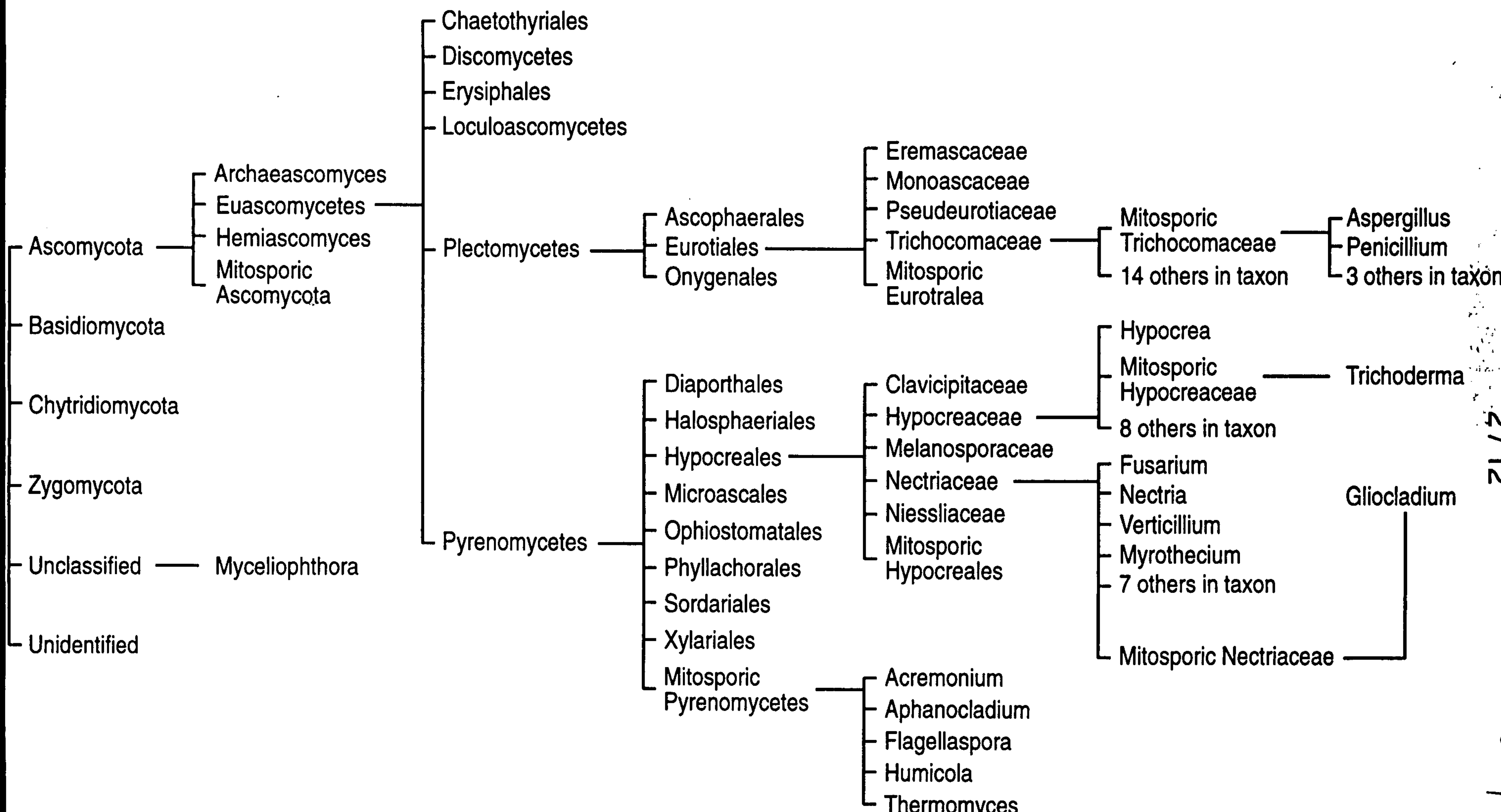

FIG._2

```
                NNLWGKDSG--GSQCTTVDSLSDGGI-SWSTAWSWSGGEGNVKSYPNS------GLQFSAGKK-VSSISS
                         10        20        30        40        50        60        70
EG3IN.PRO       NNLWGASAGS-GFGCVTAVSLSG-GA-SWHADWQWSGGQNNVKSYQNS------QIAIPQ-KRTVNSISS  60
FUSEQIN.PRO     NNFWGKDSGT-GDQCTHVNWNNANGA-GWDVEWNWSGGKDNVKSYPNS------ALLIGEDKKTISSITN  62
GLIOIN.PRO      NNKWGQGSGS-GSQCLTIDKIWDSNV-AFHADWSWSGGTNNVKSYPKR------RSEFSRGKK-VSSIGT  61
ACRHYPO.PRO     ---WGPRSAESGEQCTTNNGLSDDGTLSWSVEWIWVGAPSSVKSYPN--------VFVEAEPRPLSEVSS  59
ASPKAWA1.PRO    QNLWGEYQGT-GSQCVYVDKLSSSGA-SWHTKWIWSGGEGTVKSYSNS------GLTF-D-KKLVSDVSS  60
ASPACU1.PRO     NNLWGKDAGS-GSQCTTVNSASSAGT-SWSTKWNWSGGENSVKSYANS------GLTF-N-KKLVSQISQ  60
HUMIN.PRO       NNLWGKDTATSGWQCTYLDGTNNGGI-QWSTAWEWQGAPDNVKSYPYV------GKQIQRGRK-ISDINS  62
11AG8IN.PRO     NNRWGTSAT----QC----INVTGNGFEITQADGSVPTNGAPKSYPSVYDGCHYGNC-APRTTLPMRISS  61
ERWCARIN.PRO    NNVWGKDEI----KG-WQQTIFYNSPISMGWNWHWPSSTHSVKAYPSLVSGWHWTAGYTENSGLPIQLSS  65
GLIO314.PRO     NNLWGMGSGS-GSQCTYVDKVWAEGV-AWHTDWSWSGGDNNVKSYPYS------GRELGTKRI-VSSIKS  61
GLIO3HYP.PRO    NNLWGQDNG-SGSQCLTVEGVTDGLA-AWSSTWSWSGGSSSVKSYSNA------VLSAEAAR--ISAISS  60
HGRIS.PRO       NNLWGQDTATSGWQCTYLDGTNNGGI-QWSTAWEWQGAPDNVKSYPYV------GKQIQRGRK-ISDINS  62
RHMARIN.PRO     NNVWGAETA----QC--IEVGLETGNFTITRADH--DNGNNVAAYPAIYFGCHWAPARAIRDCAARAGAV  62
SLIVIN.PRO      NNRWGSTAP----QC----VTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYTNC-SPGTDLPVRLDT  61
PENNOT.PRO      ---WGKDSGS-GSQCASVNSISDSGV-SWSTTWNWSGGEDNVKSYPNS------GLVALK-KQPVSDISS  58
PHANHYPO.PRO    ---WGKDSG-TGSQCLTVDGISSGLL-KWSATWSWSGGPYNVKSYPNA------VLQAPAAR--ASAISS  57
F42HYPO.PRO     -----S--------QCTTFESLSGNTI-VWNTKWSWSGGQGQVKSFANA------ALQFTPKK--LSSVKS  49
EMDESHYP.PRO    NNLWGXDNADSGSQCTGVDSANGNSI-SWHTTWSWSGGSSSVKSYANA------AYQFTSTK--LNSLSS  61
MYCINS.PRO      ------------------------------------------------------------------------  1
CHBRAS.PRO      NNFWGQSRATSGSQCTYLDSSSNSGI-HWHTTWIWEGGEGEVKSYAYS------GRQVSTGLT-IASIDS  62

                IPSSASWV-YSGTDIRA-NVAYDL-FTAADPNHATSSGDYELMIW
                         80        90       100       110
EG3IN.PRO       MPTTASWS-YSGSNIRA-NVAYDL-FTAANPNHVTYSGDYELMIW                          102
FUSEQIN.PRO     MQSTAEWK-YSGDNLRA-DVAYDL-FTAADPNHETSSGEYELMIW                          104
GLIOIN.PRO      INGGADWD-YSGSNIRA-NVAYGI-FTSADPNHVTSSGDYELMIW                          103
ACRHYPO.PRO     IQAEWAWTYSGAGDFTT-NVAFDI-FTGETAD                                       89
ASPKAWA1.PRO    IPTSVTWS-QDDTNVQA-DVSYDL-FTAANADHATSSGDYELMIW                          102
ASPACU1.PRO     IPTTARWS-YDNTGIRA-DVAYDL-FTAADINHVTWSGDYELMIW                          102
HUMIN.PRO       MRTSVSWT-YDRTDIRA-NVAYDV-FTARDPDHPNWGGDYELMIW                          104
11AG8IN.PRO     IGSAPSSVSYRYTGNGVYNAAYDIWLDPTPRTNGVNR--TEIMIW                          104
ERWCARIN.PRO    NKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELMIW                          110
GLIO314.PRO     ISSGADWD-YTGSNLRA-NAAYDI-FTSANPNHATSSGDYELMIW                          103
GLIO3HYP.PRO    IPSKWEWRSYTGTDIVA-NVAYDL-FSNTDCGDTP---EYELMIW                          100
HGRIS.PRO       MRTSVSWT-YDRTDIRA-NVAYDV-FTARDPDHPNWGGDYEFMIW                          104
RHMARIN.PRO     RRAHELDVT-PI-TTGRWNAAYDIWFSPVTNSGNGYSGGAELMIW                          105
SLIVIN.PRO      VSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQ--TEIMIW                          104
PENNOT.PRO      IPSSVKWN-YDNTDIRA-DVAYDL-FTAADINHDTSSGDYE                              96
PHANHYPO.PRO    IPSKWQWESYTGSNVIA-NVAYDL-FSNSDCG                                       87
F42HYPO.PRO     IDSTWKWKSYSGSNIVA-DVAYDM-FLSTSPGGDH---NY                               84
EMDESHYP.PRO    IPTSWKWQ-YSTTDIVA-NVAYDL-FTSSSAGGDS---EYEFMIW                          100
MYCINS.PRO      ----------------A-NVAYDL-FTAADPNHATSSGDYELMIW                          27
CHBRAS.PRO      MQTSVSWE-YNTTDIQA-NVAYDI-FTAEDPDHEHSSGDYELMIW                          104
```

FIGURE 3

Percent Similarity (upper triangle) / Percent Divergence (lower triangle)

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1	EG3IN.PRO
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2	FUSEQIN.PRO
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3	GLIOIN.PRO
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4	ACRHYPO.PRO
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5	ASPKAWA1.PRO
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6	ASPACU1.PRO
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7	HUMIN.PRO
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8	11AG8IN.PRO
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9	ERWCARIN.PRO
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10	GLIO314.PRO
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11	GLIO3HYP.PRO
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12	HGRIS.PRO
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13	RHMARIN.PRO
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14	SLIVIN.PRO
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15	PENNOT.PRO
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16	PHANHYPO.PRO
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17	F42HYPO.PRO
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18	EMDESHYP.PRO
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19	MYCINS.PRO
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20	CHBRAS.PRO
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		

FIGURE 4

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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1	EG3IN.PRO
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2	FUSEQIN.PRO
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3	GLIOIN.PRO
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4	ACRHYPO.PRO
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5	ASPKAWA1.PRO
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6	ASPACU1.PRO
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7	HUMIN.PRO
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8	11AG8IN.PRO
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9	ERWCARIN.PRO
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10	GLIO314.PRO
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11	GLIO3HYP.PRO
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12	HGRIS.PRO
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13	RHMARIN.PRO
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14	SLIVIN.PRO
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15	PENNOT.PRO
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16	PHANHYPO.PRO
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17	F42HYPO.PRO
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18	EMDESHYP.PRO
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19	MYCINS.PRO
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20	CHBRAS.PRO
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		

PERCENT DIVERGENCE

PERCENT SIMILARITY

FIG._4

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FIGURE 6

```
                          1                                                           60
T._reesei                 M.........KF.LQVLPALIPAALAQTS...............CDQWATFTGNG..YTV
H._schweinitzii           M.........KF.LQVLPAILPAALAQTS...............CDQYATFSGNG..YIV
A._aculeatus__            M.........KAFHL.LAALAGAAVAQQAQ.............LCDQYATYTGGV..YTI
A._kawachii__             M.........KLSMT.LSLFAATAMGQT...............MCSQYDSASSPP..YSV
A._kawachii_2             M.........KAFHL.LAALSGAAVAQQAQ.............LCDQYATYTGGV..YTI
A._oryzae__               M.........KLSLA.LATLVATAFSQE...............LCAQYDSASSPP..YSV
H._grisei                 M........LKSALLLGAAAVSVQSASIPTIPANLEPRQIR.SLCELYGYWSGNG..YEL
H._insolens__             M........LKSALLLGPAAVSVQSASIPTIPANLEPRQIR.SLCELYGYWSGNG..YEL
Chaetomium_brasiliense    M.........KLTLVLFVSSLA......AATPLGWRERQQQVSLCGQSSSWSGNG..YQL
F._equseti                M.........KSTLLLAGAFAPLAFAKD...............LCEQYGYLSSDG..YSL
F._javanicum_1            M.........KSAIVA.ALAGLAAASPTRLIPRGQ........FCGQWDSETAGA..YTI
F._javanicum_2            M.........K..FFGVVSASLAATAVATPTTPTETIEKRDTTWCDAFGSLATSG..YTV
G._roseum____1            M.........KANIVILSLFAPLAAVAQT..............LCGQYSSNTQGG..YIF
G._roseum____2            M.........KSIISFFGLATLVAAAPSQNPTRTQPLEKRATTLCGQWDSVETGG..YTI
G._roseum____3            M.........KFQLLSLTAFAPLSLAA................LCGQYQSQSQGG..YIF
G._roseum____4            M.........KTGIAYLAAVLPLA.MAES..............LCDQYAYLSRDG..YNF
Memnoniella_echinata      M.........KVAAL.LVALSPLAF.AQS..............LCDQYSYYSSNG..YEF
Emericella_desertoru      M.........K..LLALSLVSLASAASAASIL.SNTFTRRSD.FCGQWDTATVGN..FIV
Actinomycete_11AG8        MRS......HPRS..ATM.TVLVVLASLGALLTAAAPAQANQQICDRYGTTTIQD.RYVV
S._lividans_CelB__        MRTLRPQARAPRGLLAALGAVLAAFALVSSLVTAAAPAQADTTICEPFGTTTIQG.RYVV
Rhodothermus_marinus__    MNVMR..AVLVLSLLLLFGCDWL.FPDGDNGKEPEPEPEPTVELCGRWDARDVAGGRYRV
Erwinia_carot___          MQTVNTQPHRIFRVLLPAVFSSLLLSSLTVSAASSSNDADKLYF.........GNNKYYL

                          61                                                         120
T._reesei                 SNNLWGASAGSGF..GCV.TAVSLSGG.ASWHADWQWSGGQNNVKSYQNS..........
H._schweinitzii           SNNLWGASAGSGF..GCV.TSVSLNGA.ASWHADWQWSGGQNNVKSYQNV..........
A._aculeatus__            NNNLWGKDAGSG..SQCTTVNSASSAG.TSWSTKWNWSGGENSVKSYANS..........
A._kawachii__             NQNLWGEYQGTG..SQCVYVDKLSSSG.ASWHTKWTWSGGEGTVKSYSNS..........
A._kawachii_2             NNNLWGKDAGSG..SQCTTVNSASSAG.TSWSTKWNWSGGENSVKSYANS..........
A._oryzae__               NNNLWGQDSGTGFTSQCVYVDNLSSSG.AAWHTTWTWNGGEGSVKSYSNS..........
H._grisei                 LNNLWGKDTATS.GWQCTYLDGTNNGG.IQWNTAWEWQGAPDNVKNYPYV..........
H._insolens__             LNNLWGKDTATS.GWQCTYLDGTNNGG.IQWSTAWEWQGAPDNVKSYPYV..........
Chaetomium_brasiliense    NNNLWGQSRATS.GSQCTYLDSSSNSG.IHWHTTWTWEGGEGEVKSYAYS..........
F._equseti                NNNVWGKDSGTGD..QCTHVNWNNANG.AGWDVEWNWSGGKDNVKSYPNS..........
F._javanicum_1            YNNLWGKDNAES.GEQCTTNSGEQSDGSIAWSVEWSWTGGQGQVKSYPNA..........
F._javanicum_2            YHNNWGKGDATS.GSQCTTFTSVSNNNFV.WSTSWTWAGGAGKVKSYSNV..........
G._roseum____1            NNNMWGMGSGSGS..QCTYVDKVWAEG.VAWHTDWSWSGGDNNVKSYPYS..........
G._roseum____2            YNNLWGQDNG.S.GSQCLTVEGV.TDGLAAWSSTWSWSGGSSSVKSYSNA..........
G._roseum____3            NNNKWGQGSGSGS..QCLTIDKTWDSN.VAFHADWSWSGGTNNVKSYPNA..........
G._roseum____4            NNNEWGAATGTGD..QCTYVDSTSSGG.VSWHSDWTWSGSESEIKSYPYS..........
Memnoniella_echinata      NNNMWGRNSGQGN..QCTYVDYSSPNG.VGWRVNWNWSGGDNNVKSYPYS..........
Emericella_desertoru      YNNLWGQDNADS.GSQ..TGVDSANGNSISWHTTWSWSGGSSSVKSYANA..........
Actinomycete_11AG8        QNNRWGTSAT.....QCINVT..GNGFEITQADGS..VPTNGAPKSYPSVYDGCHYG...
S._lividans_CelB__        QNNRWGSTAP.....QCVTAT..DTGFRVTQADGS..APTNGAPKSYPSVFNGCHYT...
Rhodothermus_marinus__    INNVWGAETA.....QCIEVGLETGNFTITRADHD..NGNNVA..AYPAIYFGCHWAPAR
Erwinia_carot___          FNNVWGKDEIKGWQQTIFYNSPISMG....WN..WHWPSSTHSVKAYPSLVSGWHWTAG.

                          121                                                        180
T._reesei                 .QIAIP.QKRTVNSISSMPTTASW...SYSGSNIRANVAYDL.FTAANPNHVTYSGDYEL
H._schweinitzii           .QINIP.QKRTVNSIGSMPTTASW...SYSGSDIRANVAYDL.FTAANPNHVTYSGDYEL
A._aculeatus__            .GLTF..NKKLVSQISQIPTTARW.S..YDNTGIRADVAYDL.FTAADINHVTWSGDYEL
A._kawachii__             .GLTF..DKKLVSDVSSIPTSVTW.SQD..DTNVQADVSYDL.FTAANADHATSSGDYEL
A._kawachii_2             .GLSF..NKKLVSQISHIPTAARW.S..YDNTCIRRGRAYDL.FTAADINHVTWSGDYEL
A._oryzae__               .AVTF..DKKLVSDVQSIPTDVEW.SQDFTNTNVNADVAYDL.FTAADQNHVTYSGDYEL
H._grisei                 .GKQIQRGRK.ISDINSMRTSVSW...TYDRTDLRANVAYDV.FTARDPDHPNWGGDYEL
H._insolens__             .GKQIQRGRK.ISDINSMRTSVSW...TYDRTDIRANVAYDV.FTARDPDHPNWGGDYEL
Chaetomium_brasiliense    .GRQVSTGLT.IASIDSMQTSVSW...EYNTTDIQANVAYDI.FTAEDPDHEHSSGDYEL
F._equseti                .ALLIGEDKKTISSITNMQSTAEW...KYSGDNLRADVAYDL.FTAADPNHETSSGEYEL
F._javanicum_1            .VVEI..EKKTLGEVSSIPSA..W.DWTYTGNGIIANVAYDL.FTSSTESGDA...EYEF
F._javanicum_2            .ALEK..INKKISDIKSVSTR..W.IWRYTGTKMIANVSYDL.WFAPTASSNN...AYEI
G._roseum____1            .GRELGT.KRIVSSIKSISSGADW...DYTGSNLRANAAYDI.FTSANPNHATSSGDYEV
G._roseum____2            .VLSA..EAARISAISSIPSK..W.EWSYTGTDIVANVAYDL.FSNTDCGDTP...EYEI
G._roseum____3            .GLEFSR.GKKVSSIGTINGGADW...DYSGSNIRANVAYGI.FTSADPNHVTSSGDYEL
G._roseum____4            .GLDLPE.KKIVTSIGSISTGAEW...SYSGSDIRADVAYDT.FTAADPNHATSSGDYEV
Memnoniella_echinata      .GRQLPT.KRIVSWIGSLPTTVSW...NYQGNNLRANVAYDL.FTAANPNHPNSSGDYEL
Emericella_desertoru      .AYQF..TSTKLNSLSSIPTS..W.KWQYSTTDIVANVAYDL.FTSSSAGGDS...EYEI
Actinomycete_11AG8        ...NCAPRTTLPMRISSIGSAPSSVSYRYTGNGVY.NAAYDIWLDPTPRTNGVNR..TEI
S._lividans_CelB__        ...NCSPGTDLPVRLDTVSAAPSSISYGFVDGAVY.NASYDIWLDPTARTDGVNQ..TEI
Rhodothermus_marinus__    AIRDCAARAGAVRRAHELDVTP.......ITTGRW.NAAYDIWFSPVTNSGNGYSGGAEL
Erwinia_carot___          ....YTENSGLPIQLSSNKSITSNVTYSIKATGTY.NAAYDIWFHTTDKANWDSSPTDEL

                          181                                                        240
T._reesei                 MIWLGKYGDIGPIGSS....QGTVNVGGQSWTLYYGYNGAMQV......YSFVAQT.NTT
H._schweinitzii           MIWLGKYGDIGPIGSS....QGTVNVGGQTWTLYYGYNGAMQV......YSFVAQS.NTT
A._aculeatus__            MIWLARYGGVQPIGSQ....IATATVDGQTWELWYG......ANGSQKTYSFVAPT.PIT
A._kawachii__             MIWLARYGSVQPIGKQ....IATATVGGKSWEVW..YGTSTQAGAEQKTYSFVAGS.PIN
A._kawachii_2             MIWLARYGGVQPLGSQ....IATATVEGQTWELWYG......VNGAQKTYSFVAAN.PIT
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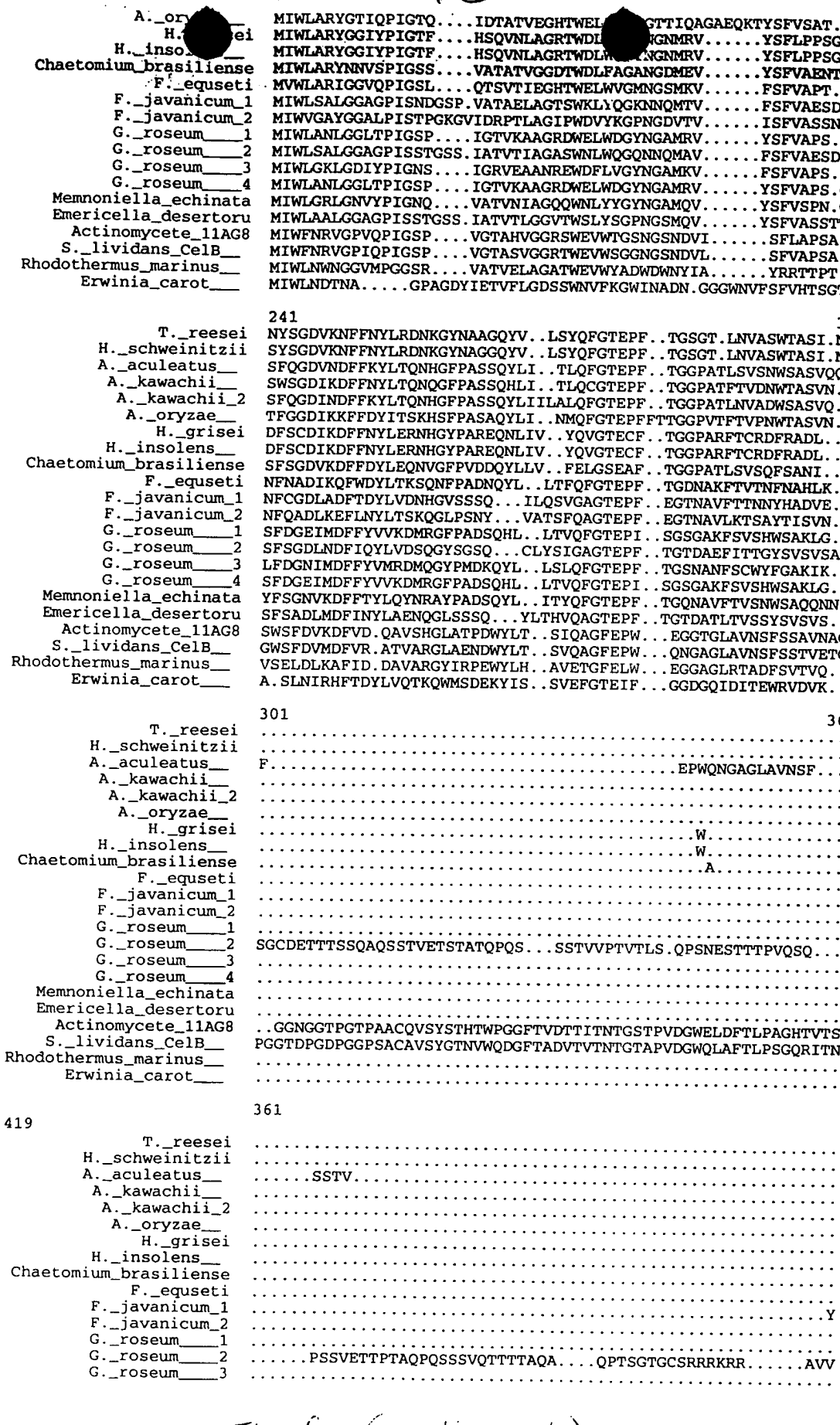

Fig 6 (continued)

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G._roseu[illegible]_4           ....................................................
Memnoniella_ec[illegible]a      ....................................................
Emericella_des[illegible]u      ....................................................
Actinomycete_[illegible]AG8     WNALISPASGAVTARSTGSNGRIAANGGTQSFGFQG[illegible]SSGTGFNAPAGGRLNGTSCTVR
S._lividans_CelB__              WNASLTPSSGSVTATGASHNARIAP.GGSLSFGFQGTYGGA.FAEPTGFRLNGTACTTV
Rhodothermus_marinus__          ....................................................
Erwinia_carot___                ....................................................
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Fig 6 (Continued)